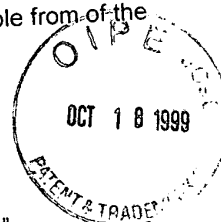


1. Application No.: 09/129,958

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s)

- ☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other



**Applicant Must Provide:**

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

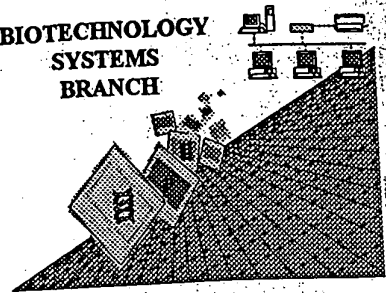
For PatentIn software help, call (703) 308-6856

**PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE**

*Fredman*

# RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number:

09/129,958

Art Unit / Team No. :

1655

Date Processed by STIC:

7/20/99



**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-30°-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/129,958

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                                 <400> sequence id number  
                                 000
- 10   ✓   Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and        which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.  
AKS-Biotechnology Systems Branch- 5/15/99

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/129,958DATE: 07/20/1999  
TIME: 16:36:07

Input Set: I129958.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

Does Not Comply  
Corrected Diskette Needed

pp 1-2

1 <110> APPLICANT: Mills, Allen P.  
2 Yurke, Bernard  
3 Platzman, Philip M.  
4 <120> TITLE OF INVENTION: ANALOG AND NEURAL NETWORK COMPUTATION USING DNA  
5 <130> FILE REFERENCE: LUTEC 0008  
6 <140> CURRENT APPLICATION NUMBER: US/09/129,958  
7 <141> CURRENT FILING DATE: 1998-08-06  
8 <150> EARLIER APPLICATION NUMBER: 09/078,761  
9 <151> EARLIER FILING DATE: 1998-05-15  
10 <150> EARLIER APPLICATION NUMBER: 09/018,248  
11 <151> EARLIER FILING DATE: 1998-02-03  
12 <150> EARLIER APPLICATION NUMBER: 60/086,654  
13 <151> EARLIER FILING DATE: 1998-05-26  
14 <160> NUMBER OF SEQ ID NOS: 4  
15 <170> SOFTWARE: PatentIn Ver. 2.0  
16 <210> SEQ ID NO 1  
17 <211> LENGTH: 10  
18 <212> TYPE: DNA  
19 <213> ORGANISM: Artificial Sequence  
20 <220> FEATURE:  
21 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA based  
22 analog oligonucleotide  
23 <400> SEQUENCE: 1 10  
24 agctatcgat  
25 <210> SEQ ID NO 2  
26 <211> LENGTH: 34  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Artificial Sequence  
29 <220> FEATURE:  
30 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA based  
31 analog oligonucleotide  
32 <220> FEATURE:  
33 <221> NAME/KEY: variation  
34 <222> LOCATION: (34)  
35 <400> SEQUENCE: 2  
36 aatgcaagat cgaaatttat acgtttatct tach  
37 <210> SEQ ID NO 3  
38 <211> LENGTH: 34  
39 <212> TYPE: DNA  
40 <213> ORGANISM: Artificial Sequence  
41 <220> FEATURE:  
42 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA based  
43 analog oligonucleotide  
44 <220> FEATURE:

W--&gt;

an explanation of "h" is mandatory  
in <223> response 34  
(see item 10 on  
Ena Summary Sheet  
and see 1.823 of sequence  
Rube,

PAGE: 2

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/129,958DATE: 07/20/1999  
TIME: 16:36:07

Input Set: I129958.RAW

45 <221> NAME/KEY: variation  
46 <222> LOCATION: (34)  
47 <400> SEQUENCE: 3 34  
48 *same error*  
aatgcaagat cgaaatttat acgtttatct tacc  
49 <210> SEQ ID NO 4  
50 <211> LENGTH: 30  
51 <212> TYPE: DNA  
52 <213> ORGANISM: Artificial Sequence  
53 <220> FEATURE:  
54 <223> OTHER INFORMATION: Description of Artificial Sequence: DNA based  
55 analog oligonucleotide  
56 <400> SEQUENCE: 4 30  
57 aatgcaagat cgaaatttat acgtttatct

VERIFICATION SUMMARY  
PATENT APPLICATION US/09/129,958

DATE: 07/20/1999  
TIME: 16:36:07

Input Set: I129958.RAW

Line	Error/Warning	Original Text
36	W "N" or "Xaa" used: Feature required	aatgcaagat cgaaatttat acgtttatct tacn
48	W "N" or "Xaa" used: Feature required	aatgcaagat cgaaatttat acgtttatct tacn